

CDC7 Gene Structure

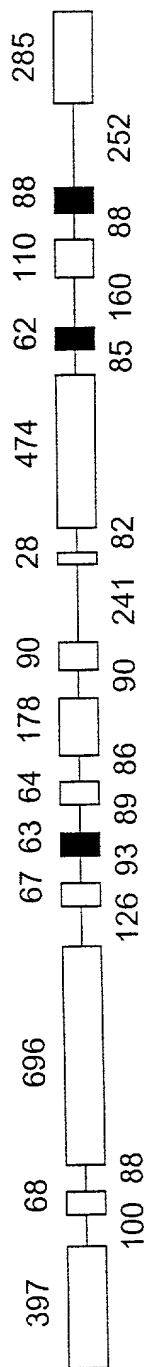


FIGURE 1

CDC27A1 Gene Structure

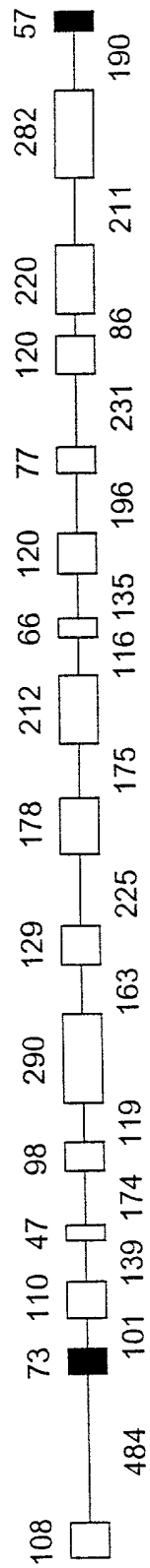


FIGURE 2

Fig. 3

1 ATGTCAGAAAACTCGGAACCGCGTCAACTCGAGAATTCAC 60
 TCTAAGTGTCTGTAACGTTACAGTCTTTTGAGCCTTGGCGCAGTTGAGCTCTTAAGATGT
 M S E N S E P R Q L E N S T -
 61 GCCGGAAGAGAGCTCATTCTCTTAGTCCCACCAATTCAGACGGCAACGACGACCTTAAC 120
 CGGCCCTTCTCTCGAGTAAGGAGAATCAGGGTGGTTAAGTCTGCCGTTGCTGCTGGAATTG
 A G R E L I P L S P T N S D G N D D L N -
 121 TATCATCTGCATGCTTTTGGAGTTATCTCGTCTCCTACTTTCTTCTGGTCATCCAGAATCT 180
 ATAGTAGACGTACGAAAACTCAATAGAGCAGAGGATGAAAGAAGACCAGTAGGTCTTAGA
 Y H L H A F E L S R L L L S S G H P E S -
 181 GTTATAGATCTTTCTTCAAAGTGTACATACTTCCAAGGTTCTCCTAATCTCGTCAAATAT 240
 CAATATCTAGAAAGAAGTTTCAATGTATGAAGGTTCCAAGAGGATTAGAGCAGTTTATA
 V I D L S S K C T V F Q G S P N L V K Y -
 241 CTTTGGCTCGATCCCTAATTCCTCTATTTCCCTTGGCGAAGATGGCTTCAGTGTGACTCTC 300
 GAAACGAGCTAGGGATTAAAGAGGATAAAGGGAACGGCTTCTACCGAAGTGACACTGAGAG
 L C S I P N S P I S L A E D G F T V T L -
 301 TCGCCTGAGTCTCCCTCCGCTCCGGCTAGTTTCGGCCTGTAGTTTGGATTTCAGGAAAT 360
 AGCGGACTCAGAGGGAGGCGAGGCCGATCAAAGCGGACATCAAACCTAAACGTCCTTTTA
 S P E S P S A P A S F A C S L D L Q E N -
 361 GTTGTGTTAGAACAGTTTATGGATCCGAGATCTCTCAGGCTAAAGCATTCCAGAGAGAAT 420
 CAACACAATCTTGTCAAATACCTAGGCTCTAGAGAGTGCGATTTCGTAAGCTCTCTCTTA
 V V L E Q F M D P R S L T L K H S R E N -
 421 GCCGAACAAGAGGAGCTAGAGCTCATGCCATTGCCCAAAAGAAGTCGAAATGATGGAAAC 480
 CGCCTTGTCTCCTCGATCTCGAGTACGGTAACGGGTTTTCTTCAGCTTTACTACCTTTG
 A E Q E E L E L M P L P K R S R N D G N -

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481 743
 GATGTGAATTACTCTGTAATAGATAGCGACCTTAACGACATCGAAGCTGTTCCTGGGA
 540
 CTTACCTTAATGAGACATTTATCTATCGTCTGGATTGCTGTAGTCTTGAACCGACACCT
 743
 D V N Y S V I D S R E N D I R T V A C G -
 541
 ACTATGCTTGGGACTATTTTATGCTCTTGAATCCCAAGCTTCGGTCTTCAATTAAAGTGC
 600
 TGATACGAACCCCTGATAAAATCGAGAACTTAGGGTTCGAAGCCAAAAGTTAAATTCACGT
 T M L G T I L A L E S Q A S V F N L S A -
 601
 TCTAACCGAGGAATAGAGGCTTTTGTTCAGATCATCAGCCTGGTCCGCGAGACATCCAAAT
 660
 AGATTGGCTCCTTATCTCCGAAAACAAGTTCTAGTAGTCCGACCCGGCGTCTGTAGGTTA
 S N R G I E A F V Q D E Q P G P Q T S N -
 661
 GCTTCAGTGGATGTCAATCCTACACATCGGTTAGAGGAAAGCAAGAACGATTTGCCATCT
 720
 CGAAGTCCACCTACAGTTAGGATGTGTAGCCCAATCTCCTTTCTTCTGCTAAACGGTLAGA
 A S V D V N P T H R L E E S K N D L P S -
 721
 COTCAGGAGGATGGATATTACGAGCGACCTGAAATTGGAGATTTCCAAATGTCTGACAAC
 780
 GGAGTCCCTCCTACCTATAATGCTCGCTGGACTTTAACCTCTAAAGGTTTAAACGCTGTG
 P Q E D G Y Y E R P E I G D F Q I A D N -
 781
 CAAATATTAAATCGAAGAAGGTGATGATAAAAAATAAGAAGGATCTCTTCCCTAAGGGAGAG
 840
 GTTTATAATTAGCTTCTTCCACTACTATTTTATTTCTTCTTCTAGAGAAGGGATCCCTCTC
 Q I L I E E G D D K N K K D L F P K G E -
 841
 ATACAAACTGATTCTGTGCACTCCGATCCCGTTGCCTCATTCATGCCAACAGAAATGAG
 900
 TATGTTTGAAGACACCTCAGGCTAGGGCAACCGAGTAACCTACGGTTGTCTTTTACTC
 I Q T D S V Q S D P V A S L M P T E N E -
 901
 TTAGAACCAGTGCAGATTGTGGATGACACTGAAGATCTACTTGTAGATGATCACACTGTA
 960
 AATCTTGGTCACTCTAACACCTACTGTGACTTCTAGATGAACATCTACTAGTGTGACAT
 L E P V Q I V D D T E D L L V D D H T V -
 961
 GACATCGTTAGCACCCCTGACAGAGAGCTGCCCTTGAAGCCTTCTGCTACAGAAGCTAAT
 1020
 CTGTAGCAATCGTGGGCACTGTCTCTCGACCGCAACTTTCGGAAGACGATGTCTTCGATTA
 D I V S T P D R E L P L K P S A T E A N -
 1021
 CAAGATAAATCTTTGGTACAAAAAACTCTGGATCAATGCAAAATTGCCGGGAAACAGCAAA
 1080
 GTTCTATTTAGAAACCATGTTTTTTTGAGACCTAGTTACGTTTAAACGGCCCTTTGTCTTT

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Q D K S L V Q K T L D Q C K L F G N S K -
ACGTACAGCTGTTCCCTGAGATAAAACACACCAGAAAAGTAAAGTTATCCAGAAGAGG 1140
TGCATGTCGACAAGGGGACCTATTTTGGTGGTCTTTTTCATTTCATAGGTCTCTCTCC
T Y S C S P E I K H T R K S K V I Q K R -
AAGCAGAATTTTAAACACCGTTTCGTCTTAAAGATCAGAAGCATCAGGCAAGCATACACA 1200
TTCGTCTTAAATTTGTGGCAAGCAGAAATTTCTAGTCTTCTAGTCCGTTTTCGTATTGEGT
K Q N F N T V R L K D Q K D Q A K H N T -
ATTCCAGATTTTGGATTCTTACACTATTGTAGAGGAAGAGGTTTCAGGTGGCTACGGGATT 1250
TAAGGTCTAAAACTAAGAATGTGATAACATCTCTCTTCCAAGTCCACCGATGCCCTAA
I P D F D S Y T I V E E E G S G G Y G I -
GTTTTATAAGGCAACGAGGAAAACCTGATGGAACAGAGTTTGCATTTAAATGCCCTCATGTT 1320
CAAATATTCCGTTGCTCTCTTTTGACTACCTTGTCTCAAACGTTAATTTACGGGAGTACAA
V Y K A T R K T D G T E F A I K C P H V -
GGCGCTCAGAAGTATTATGTAATAATGAATCAGAATGCTGGAGCGTTTGGGGGAAA 1380
CCGCGAGTCTTCATAATACACTTATTACTTTAGTCTTACGACCTCGCAAAACCCCTTTT
G A Q K Y Y V N N E I R M L E R F G G K -
AACTGTATAATAAAGCATGAAGGCTGTCTCAAGAATGGAGATTCTGATTGCATCATCTTT 1440
TTGACATATTATTTTCGTACTTCCGACAGAGTTCTTACCTCTAAGACTAACGTAGTAGGAA
N C I I K H E G C L K N G D S D C I I L -
GAGCACCTTGAACATGACAGACCTGATTCAATGAAGAGAGAAATAGATGTGTATCAGCTG 1500
CTCGTGGAACCTTGTACTGTCTGGACTAAGTAACTTCTCTCTTTATCTACACATAGTCGAC
E H L E H D R P D S L K R E I D V Y Q L -
CAGTGGTACGGCTACTGCATGTTCAAAGCTCTATCGAGTCTGCATAAGCAGGGTGTGTT 1560
GTCACCATGCCGATGACGTACAAGTTTTCGAGATAGCTCAGACGTATTCTTCCCACAACAA
Q W Y G Y C M F K A L S S L H K Q G V V -
CATAGGGATGTTAAGCCAGGAAACTTCTCTCTCTAGGAAGACCAACAAAGGCTATCTC 1620
GTATCCCTACAAATTCGGTCTCTTGAAGGAGAAGAGATCTTCTGGTTGTTTCCGATAGAG
H R D V K P G N F L F S R K T N K G Y L -
ATTGATTTTAACTTGGCATGATTTTGCACCAGAAGTACAGAAGAGCAGATAAATCAAAA

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1621 ----- 1680
TAACTAAAAATTGGACCGGTACCTTAAACGTTGGTCTCTGTCCTTCTCGTCTATTAGTTTT
8|9 3|10
I D F N L A M | D L H Q K Y R R A D | K S K -
GCAGCTTCAGGTCTTCCCTACCGCCAGCAAGAACTTCATTCATTGGTTAAATCACTCCAT
1681 ----- 1740
CGTCCAGTCCAGAGGATGGCCGGTCTTCTTGTAGTATGTAACCAATTAGTGAGCTA
A A S G L P T A S K K E E T L V K S L D -
GCGGTAAACCGAGGGACCAACAAACCTTCTCAGAAAACCTTAGCCCTAATAGTATCAG
1741 ----- 1800
CGCCATTGGCTCCCTGGTGTGTTTGAAGAGTCTTTTGAAATCGCGGATTATCATAGTTC
A V N R G T N K P S Q K T L A P N S I K -
AAAGCAGCGGGAAAGACAAGAGCTCGGAATGACATGACCAGATGGGAGAGACTCAATAGC
1801 ----- 1860
TTTCGTCCGCTTTCTGTTCTCGAGCCCTTACTGTACTGGTCTACCTCTCTGAGTTATCG
K A A G K T R A R N D M T R W E R L N S -
CAAGGGGCAGAAGGTTCTGGCTTAACTTCAGCTAAAGATGTGACCAGCAAGGAACAAC
1861 ----- 1920
GTTCCCCCTCTTCCGACCCGAATTGAAGTCGATTTCTACACTGGTCTGTTCCTTGTTG
Q G A E G S G L T S A K D V T S T R N N -
CCTTCAGGTGAAAAGAGAAGAGAGCCCTTGGCATGTGATGGAAGAAAAGCGCTTTTAGAT
1921 ----- 1980
GGAAGTCCACTTTTCTTCTCTCGGAAACGGTACAGTACCTTCTTTTCGCGAAAATCTA
P S G E K R R E P L P C H G R K A L L D -
TTTCTGCAAGAGACAATGTCTGTTCCAAATTCGAAACCATGAAGTATCATCCAAAGCTCCT
1981 ----- 2040
AAAGACGTTCTCTGTACAGACAAGGTTAAGGTTGGTACTTCATAGTAGGTTTCGAGGA
F L Q E T M S V P I P N H E V S S K A P -
ACGTCTATGAGAAAACGGGTAGCTGCTCTTCCAGGGAAAGCTGAGAAGGAACCTTCTTTAT
2041 ----- 2100
TGCAGATACTCTTTTGGCCATCGACGAGAAGTCCCTTTTCACTCTTCTTGAAGAAATA
T S M R K R V A A L P G K A E K E L L Y -
CTGACCCCAATGCCACTGTGCTCTAACGGTCCGCTGAAGCAGGGGACGTAATTGAGAAG
2101 ----- 2160
GACTGGGGTTACGGTGACACGAGATTGCCAGCCGGACTTCGTCCCCTGCATTAACCTCTC
10|11
L T P M P L C S N G R P E A G | D V I E K -
11|12
AAAGACGGTCTTTGCTCAGGAACCAAGGCTTCCGAGCTCCAGAGGTTTGCTTCAGATCT
2161 ----- 2220
TTTCTGCCAGGAACGAGTCTTTGGTTTCCGAAGGCTCGAGGTCTCCAACGAAGTCTAGA
11|12
K D G P C S G T K G F R A P E | V C F R S -

2221 TGGCACCAGGACCTAAGATGACGCTGGGTCTGGCGGGAGTTA¹²CTTTGTTTATACCTTCATA 2280
 AACGTTGGTTCCTGGATTCTATCTGTGACACCGACCGCCCTCAATGAAACAATATGGAGTAT
 L H Q G E K I D V W S A G V T L L Y L I -
 2281 ATGGGAAGGACACCTTTCACTGGTGA¹²CCCTGAAC¹³GAACATAAAGGACATTGGCACAACCTA 2340
 TACCCCTTCCTGTGGAAAGTGACCACTGGGACTTGTCTGTATTTCCTGTAAACGTTGTGAT
 M G R T P F T G D E E Q¹² N I K D I A Q L -
 2341 CGAGGCAGTGAAGAATTATGGGAAGTAGCCCAAGCTGCCCAACCGTGAATCCTCTTTCCCT 2400
 GCTCCGTCACCTTCTTAATACCCCTTCATCGGTTCCGACGTTGTTGGCACTTAGGAGAAAGGGA
 R G S E E L W E V A K L H N R E S S E P -
 2401 AAGGAATTATACGAGTCAAGGTACTTGAAGGGGATGGAGTTGAGAAAATGGTGGCAACTC 2460
 TTCTTAATATGCTCAGTTCATGAACCTTCCCTACCTCAACTCTTTTACCAAGCTTGAG
 K¹³ E L Y E S R Y L K G M E I R K W C E L -
 2461 AACACAAAACGCAGAGAGTTTCTAGACGTAATTCCACTATCGCTTCTTGACCTCGTTGAT 2520
 TTGTGTTTTTGGTCTCTCTCAAGATCTGCAATTAAGGTGATAGCGAAGAACTGGAGCAACTA
 N T K R R E F L D V I P L S L L D L V D -
 2521 AAATGTTTGACCGTTAACCCGAGGCSACGAATCAGCGCAGAGGATGCTCTCAAGCACGAC 2580
 TTTACAAACTGGCAATTGGGCTCCGCTGCTTAGTCCGCTCTCCTACGAGAGTTCTGTGCTG
 K C L T V N P R R R I S A E D A L K H D -
 2581 TTCTTCCATCCAGTACATGAAACCCCTTAGAAACCAATGCTCCTTAAACAGCAGCCTTACA 2640
 AAGAAGGTAGGTCACTACTTTGGGAATCTTTGGTTTACGAGGAATTTGTGCTCGGATGT
 F F H P V H E T L R N Q M L L K Q Q P T -
 2641 GTGGTTGCTGACCGCAGTAAGCCAAACTCTAAACTATTTACAATTGTAA¹⁴AAGTAAATAAG 2699
 CACCAACGACTGCCTCATTCGGTTTGAGATTTCATAAATGTTAACATTTTCATTTATTC
 V V A D A V S Q T L N Y L Q L *

[illegible]

1 60
CCGCTGTAATGTGTGTGTGTCGGAGGCTCCCTTGTTGTGTGTGTAGCTAACAGAGCAGTTAAA
61 120
ATGATGGAGAATCTACTGGCGAATTGTGTCCAGAAAAACCTT
CCAGTAGTAGTAGTAGTCTACTACCTCTTAGATGACCGCTTAACACAGGTCTTTTGGAA
121 180
M M E N L L A N C V Q K N L
AACCATTTTATGTTTCACCAATGCTATCTTCCTTTGCGAAGTTCTTCTCGGCCCAATTTCCA
181 240
TTGGTAAAATACAAGTGGTTACGATAGAAGGAAACGCTTGAAGAAGAGCGGGTTAAAGGT
N H F M E T N A I E L C E L L L A Q F P
241 300
TCTGAGGTGAACCTGCAATTGTTAGCCAGGTGTTACTTTCAGTAACAGTCAAGCTTATAGT
AGACTCCACTTGGACGTTAACAATCGGTCCACAATGAAGTCAATGTCAGTTCCGAATATCA
301 360
S E V N L Q L L A R C Y L S N S Q A Y S
GCATATTATATCCTTTAAAGGTTCAAAAAACGCTCAGTCTCGGTATTTTATTTGGATTCTCA
361 420
CGTATAATATAGGAATTTCCAAGTTTTTTCGGAGTCCAGAGCCATAAATAAACGTAAGAGT
A Y Y I L K G S K T P Q S R Y L F A F S
TGCTTTAAGTTGGATCTTCTTGGAGAGGCTGAAGCTGCATTGTTGCCCTGTGAGATTAT
421 480
ACGAAATTCAACCTAGAAGAACCTCTCCGACTTCCAGCTAACCAACGGGACACTTCTAATA
C F K L D L L G E A E A A L L P C E D Y
481 540
GCTGAAGAAGTTCTGTTGGTGCAGCTGGGCATTATCTTCTTGGTCTTATATATAGATAT
541 600
CGACTTCTTCAAGGACCACCAGTCCGACCCGTAATAGAGAACCAGAATATATATCTATA
A E E V P G G A A G H Y L L G L I Y R Y

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TCTGGGAGGAAGAACTGTTCAATACAACAGTTTAGGATGGCATTGTCATTTGATCCATTG
421 ----- 480
AGACCCCTCCTTCTTGACAAGTTATGTTGTCAAATCCTACCGTAACAGTAAACTAGGTAAC

S G R K N C S I Q Q F R M A L S F D P L
516
TGTGGGAAGCATATGGGAACTTTGTAGTTTAGTGGCGCTGAAGAAGCCTCAACAGTT
481 ----- 540
ACAACCCCTTCGTATACCTCTTGAAACATCAAATCCACGGCGACTTCTTCGGAGTTGTCAA
516
C W E A Y G E L C S L G A A E E A S T V

TTCGGGAATGTTGCTTCCCAGCGTCTTAAAACTTGTGTAGAACAAGAATAAGCTTCTCA
541 ----- 600
AAGCCCTTACAACGAAGGGTTCGCAGAATTTTGAACACATCTTGTTCCTTATTCGAAGAGT

E G N V A S Q R L K T C V E Q R I S F S

GAAGGAGCAACCATAGACCAGATTACAGATTCTGATAAGGCCTTAAAAGATACAGGTTTA
601 ----- 660
CTTCCTCGTTGGTATCTGGTCTAATGTCTAAGACTATTCCGGAATTTTCTATGTCCAAT

E G A T I D Q I T D S D K A L K D T G L

TCGCAAACAGAACACATTCCAGGAGAGAACCAACAGATCTGAAAATTATGCAGCAGCCT
661 ----- 720
AGCGTTTGTCTTGTGTAAGGTCCTCTCTTGGTTGTTCTAGACTTTTAAATACGTCGTCGGA

S Q T E H I P G E N Q Q D L K I M Q Q P

GGAGATATTCCACCAAATACTGACAGGCAACTTAGTACAAACGGATGGGACTTGAACACA
721 ----- 780
CCTCTATAAGGTGGTTTATGACTGTCCGTTGAATCATGTTTGCCTACCCCTGAACTTGTGT

G D I P P N T D R Q L S T N G W D L N T
617
CCTTCTCCAGTGCTTTTACAGGTAATGGATGCTCCACCGCCTCTGCTTCTTAAGAATATG
781 ----- 840
GGAAGAGGTCACGAAAATGTCCATTACCTACGAGGTGGCGGAGACGAAGAATTCTTATAC
617
P S P V L L Q V M D A P P P L L L K N M

CGTCGTCCAGCAGTGGAAGGATCTTTGATGTCTGTACATGGAGTGGTGTGCGTCCAAGA
841 ----- 900
GCAGCAGGTCGTCACCTTCCTAGAACTACAGACATGTACCTCACGCACACGCAGCTTCT

R R P A V E G S L M S V H G V R V R R R

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7⁸
901 AACTTTTTGTGAAGAATTGTCAGCAGAGGCTCAAGAAGAATCTGGGGCGCCGCCGTAGT 960

TTGAAAAAATCACTTCTTAACAGTCGTCTCCGAGTTCTTCTTAGACCCCGCGCGGCATCA
7⁸
N F F S E E L S A E A Q E E S G R R R S
GCTAGAATAGCAGCAAGGAAAAAGAATCCTATGTGCGCAGTCATTGCGAAAAGATTCCCAT
961 ----- 1020
CGATCTTATCGTCGTTCTCTTTTCTTAGGATACAGCGTCAGTAAACCTTTTCTAAGGGTA
A R I A A R K K N P M S Q S F G K D S H
TGTTTACATCTTTTACCTTCCGAGTCAAACATATGCACCTTCTCTTCTCGATGATTGGA
1021 ----- 1080
ACCAATGTAGAAAGTGAAGGCTCAGTTTGATACGTGGAAGAGAAAGGAGCTTAACTT
W L H L S P S E S N Y A P S L S S M I G
8⁹
1081 AAATGCAGAATCCAAAGCAGCAAAGAAGCGATTCTGTATACCGTTACTCTAAATGATCCA 1140

TTTACGTCTTAGGTTTTCGTCTTTTCTTCGCTAAGGACTATGGCAATGAGATTACTAGGT
8⁹
K C R I Q S S K E A I P D T V T L N D P
GCAACGACGTCAGGCCAGTCTGTAAAGTGACACTGGAAGCTCTGTTGATGATGAGGAAAAG
1141 ----- 1200
CGTTGCTGCAGTCCGGTCAGACATTCACTGTGACCTTCGAGACAACTACTACTCTTTTTC
A T T S G Q S V S D T G S S V D D E E K
TCAAATCCTAGTGAATCTTCCCCGGATCGTTTTCAGCCTTATTTCTGGAATTTTCAAGAGTG
1201 ----- 1260
AGTTTAGGATCACTTAGAAGGGGCTAGCAAAGTCGGAATAAAGACCTTAAAGTCTTCAC
S N P S E S S P D R F S L I S G I S E V
CTAGGCATTCTGAAAATTCTTGGAGATGGCCACAGGCATTTACATATGTACAAGTGTGAG
1261 ----- 1320
GATCCGTAAGACTTTTAAGAACCTCTACCGGTGTCCGTAAATGTATACATGTTTCACAGTC
9
L G I L K I L G D G H R H L H M Y K C Q
9

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1321 GAAGCTTTTGGTCATATCAAAAGCTATCTCAGAAACATACAATACACACTGGGTTCTC 1380
CTTCGAAACAACCGTATAGTTTTCCGATAGAGTCTTTGTTATGTTATGTGTGACCCCAAGAG
1381 E A L L A Y Q K L S Q K Q Y N T H W V L
ATGCAGTTTGGAAAAGCATATTTTGGAGCTACAAGACTACTTCAACGCTGACTCTTCTCTT
TACGTCCAACCTTTTTCGTATAAAACTCGATGTTCTGATGAAGTTGCCGACTGAGAAGGAAA 1440
M Q V G K A Y F E L Q D Y F N A D S S F
ACTCTTGCTCATCAAAAGTATCTCTTATGCTTTTGGGAAGGAATGGATACATACTCCACTGTT
1441 TGAGAACGAGTAGTTTTCATAGGAATACGAAACCTTCTTACCTATGTATGAGGTGACAA 1500
T L A H Q K Y P Y A L E G M D T Y S T V
CTTTATCACCTGAAAGAAGAGATGAGGTTGGGCTATCTGGCTCAGGAACTGATTTTCAGTT
1501 GAAATAGTGGACTTTTCTCTCTACTCCACCCGATAGACCGAGTCTTTGACTAAAGTCAA 1560
L Y H L K E E M R L G Y L A Q E L I S V
GATCGCTGTCTCCAGAATCCTGCTGTGTCAGTTGGGAACTGTTACAGTTTGCCTAAGGAT
1561 CTAGCGGACAGAGGTCTTAGGACCAACGTCACCCCTTGACCAATGTCAAACGCAATTCCTA 1620
D R L S P E S W C A V G N C Y S L R K D
CATGATACTGCTCTCAAAATGTTTTCAGAGAGCTATCCAACCTGAATGAAAGATTACATAT
1621 GTACTATGACGAGAGTTTACAAAGTCTCTCGATAGGTTGACTTACTTTCTAAGTGTATA 1680
H D T A L K M F Q R A I Q L N E R F T Y
GCACATACCCCTTTGTGGCCACGAGTTTGGCCGATTTGGAAGAATTGAGGATGCAGAGAGA
1681 CGTGTATGGGAAACACCGGTGCTCAAACGGCGTAACCTTCTTAAGCTCCTACGTCTCTCT 1740
A H T L C G H E F A A L E E F E D A E R
TGCTACCGGAAGGCTCTGGGCATAGATACGAGACACTATAATGCATGGTACGGTCTTGGGA
1741 ACCATGGCCTTCCGAGACCCGATCTATGCTCTGTGATATTACGTACCATGCCAGAACCT 1800
C Y R K A L G I D T R H Y N A W Y G L G -

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1801 ATGACCTATCTTCGTCAGGAGAAATTCGAGTTTGCGCAGCATCAATTTCAACTGGCTCTC 1860
TACTGGATAGAAGCAGTCCTCTTTAAGCTCAAACGCGTCGTAGTTAAAGTTGACCGAGAG
M T Y L R Q E K F E F A Q H Q F Q L A L
1861 CAAATAAATCCAAGATCTTCAGTCATCATGTGTTACTATGGAATTGCTTTGCATGAGTCA 1920
GTTTATTTAGGTTCTAGAAGTCAGTAGTACACAATGATACCTTAACGAAACGTACTCAGT
Q I N P R S S V I M C Y Y G I A L H E S
1921 AAGAGAAACGATGAGGCGTTGATGATGATGGAGAAGGCTGTACTCACTGATGCAAAGAAT 1980
TTCTCTTTTGCTACTCCGCAACTACTACTACCTCTTCGACATGAGTGACTACGTTTCTTA
K^{14/15} R N D E A L M M M E K A V L T D A K N
1981 CCGCTCCCCAAGTACTACAAGGCTCACATATTAACCAGCCTAGGTGATTATCACAAGCA 2040
GGCGAGGGGTTTCATGATGTTCCGAGTGTATAATTGGTCCGATCCACTAATAGTGTTCGT
P L P K Y Y K A H I L T S L G D Y H K A
2041 CAGAAAGTTTTAGAAGAGCTCAAAGAATGTGCTCCTCAAGAAAGCAGTGTCCATGCATCG 2100
GTCTTTCAAATCTTCTCGAGTTTCTTACACGAGGAGTTCTTTCGTACAGGTACGTAGC
Q K V L E E L K E C A P Q E S S V H A S
2101 CTTGGCAAAATATACAATCAGCTAAAGCAATACGACAAAGCCGTGTTACATTTCCGGCATT 2160
GAACCGTTTTATATGTTAGTCGATTTTCGTTATGCTGTTTCGGCACAATGTAAAGCCGTAA
L G K I Y N Q L K Q Y D K A V L H F G I
2161 GCTTTGGATTTAAGCCCTTCTCCATCTGATGCTGTCAAGATAAAGGCTTACATGGAGAGG 2220
CGAAACCTAAATTCGGGAAGAGGTAGACTACGACAGTTCTATTTCCGAATGTACCTCTCC
A L D L S P S P S D A V K I K^{15/16} A Y M E R

	TTGATACTACCGACGAGCTGGTGCACGGAGGAAAAATTTGTAGATTATTTGTGTCAGGTAAT	
2221	-----	2280
	AACTATGATGGTCTGCTCGACCACTGCCTCCTTTTAAACATCTAAATACACGTCCTCATTA	
	L I L P D E L V T E E N L *	
	ACACCGAGATTATGTTTTCTCATATAACCCAAAGTCATCTGTAATTTTTTCTCATCTTTTAGAT	
2281	-----	2340
	TGTGGTCTAAATACAAACAGTATATTGGGTTTCAGTAGACATTAATAAAGAGTAGAAATCTA	
	
	CAGTCTTGTGGACTAACCCTAAAAACAAAACCTGATTATATAAACTTAGAGGGTAATATTAC	
2341	-----	2400
	GTCAGAACACCTGATTGGGATTTTTGTTTTGACTAATATATTTGATCTCCCATTTATATG	
	
	AGAAAAATTGTATAGAGTTGGGTTTTGAAATTTTCAATTTCTTTTCCAAAGTTGGAACTTTTGT	
2401	-----	2460
	TCCTTTTAACTATCTCAACCCAAAACCTTAAAAAGTAAAGAAAAGGTTCAACCTTGAAAACAA	
	
	CAA	
2461	-----	2512
	GTT	
	

Variable	Mean	SD	Min	Max
Age	35.2	10.5	18	65
Gender	50.0	50.0	0	100
Marital status	65.0	48.0	0	100
Education	12.5	2.0	8	16
Income	30.0	15.0	10	50
Occupation	25.0	20.0	0	100
Health status	70.0	10.0	50	90
Stress level	45.0	15.0	20	70
Life satisfaction	60.0	12.0	40	80
Resilience	55.0	18.0	30	80
Optimism	65.0	14.0	45	85
Gratitude	70.0	16.0	50	90
Forgiveness	60.0	15.0	40	80
Empathy	65.0	17.0	45	85
Compassion	70.0	19.0	50	90
Kindness	75.0	20.0	55	95
Generosity	80.0	21.0	60	100
Patience	85.0	22.0	65	100
Humility	90.0	23.0	70	100
Modesty	95.0	24.0	75	100
Shamelessness	100.0	25.0	80	100
Indifference	105.0	26.0	85	100
Disrespect	110.0	27.0	90	100
Disobedience	115.0	28.0	95	100
Disloyalty	120.0	29.0	100	100
Disrespectfulness	125.0	30.0	105	100
Disobedience	130.0	31.0	110	100
Disloyalty	135.0	32.0	115	100
Disrespectfulness	140.0	33.0	120	100
Disobedience	145.0	34.0	125	100
Disloyalty	150.0	35.0	130	100
Disrespectfulness	155.0	36.0	135	100
Disobedience	160.0	37.0	140	100
Disloyalty	165.0	38.0	145	100
Disrespectfulness	170.0	39.0	150	100
Disobedience	175.0	40.0	155	100
Disloyalty	180.0	41.0	160	100
Disrespectfulness	185.0	42.0	165	100
Disobedience	190.0	43.0	170	100
Disloyalty	195.0	44.0	175	100
Disrespectfulness	200.0	45.0	180	100
Disobedience	205.0	46.0	185	100
Disloyalty	210.0	47.0	190	100
Disrespectfulness	215.0	48.0	195	100
Disobedience	220.0	49.0	200	100
Disloyalty	225.0	50.0	205	100
Disrespectfulness	230.0	51.0	210	100
Disobedience	235.0	52.0	215	100
Disloyalty	240.0	53.0	220	100
Disrespectfulness	245.0	54.0	225	100
Disobedience	250.0	55.0	230	100
Disloyalty	255.0	56.0	235	100
Disrespectfulness	260.0	57.0	240	100
Disobedience	265.0	58.0	245	100
Disloyalty	270.0	59.0	250	100
Disrespectfulness	275.0	60.0	255	100
Disobedience	280.0	61.0	260	100
Disloyalty	285.0	62.0	265	100
Disrespectfulness	290.0	63.0	270	100
Disobedience	295.0	64.0	275	100
Disloyalty	300.0	65.0	280	100
Disrespectfulness	305.0	66.0	285	100
Disobedience	310.0	67.0	290	100
Disloyalty	315.0	68.0	295	100
Disrespectfulness	320.0	69.0	300	100
Disobedience	325.0	70.0	305	100
Disloyalty	330.0	71.0	310	100
Disrespectfulness	335.0	72.0	315	100
Disobedience	340.0	73.0	320	100
Disloyalty	345.0	74.0	325	100
Disrespectfulness	350.0	75.0	330	100
Disobedience	355.0	76.0	335	100
Disloyalty	360.0	77.0	340	100
Disrespectfulness	365.0	78.0	345	100
Disobedience	370.0	79.0		

CDC27B Gene Structure

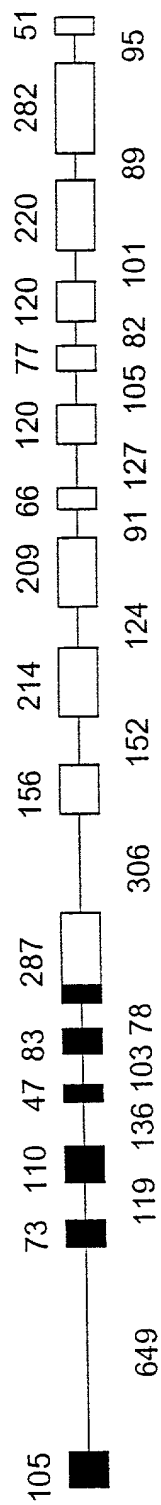


FIGURE 5

SEQ ID NO 6

Cdc27A1 1- MMENLLANCVQKNLNHFMTNAIFLCELLLAQFPSEVNLQLLARCYSNS
Cdc27B 1- MEAMLV-DCVNNSLRHFVYKNAIFMCERLCAEFPSEVNLQLLATSYLQNN

SEQ ID NO 10

SEQ ID NO 6

Cdc27A1 51- QAYSAYVILKGSKTPOSRYLFAFSCEKLDLLGEAFAALLP-CEDYAEVVP
Cdc27B 50- QAYSAYHLLKGTQMAQSRYLFAFSCEQMDLLNEAESALCPVNEPGAE-IP

SEQ ID NO 10

Cdc27A1 100- GGAAGHYLLGLIYRYSGRKNCISIQFRMALSFDPWCWEAYGELCSLGAAE
Cdc27B 99- NGAAGHYLLGLIY----KKNAA-QQFKQSLTIDPLLWAAYEELCILGAAE

SEQ ID NO 10

Cdc27A1 150- EASTVFGNVASQRLQKTCVEQRISFSEG-ATIDQ--ITDSKAL--KDTG
Cdc27B 144- EATAVFGETAALSIQKQYMQQ-LSTSLGLNTYNEERNSTSTKNTSSSEDYS

SEQ ID NO 10

Cdc27A1 194- LSQTEHIPGENQDDLKIMQQPGDIPPNTDRQLSTNGWDLNTPSPVLLQVM
Cdc27B 193- PROSKHTQSHGLKDISGNFHSBGVNGGV----SNMSFY-NTPSPVAAQLS

Cdc27A1 244- D-APPPLLL NMRRPAV-EG-SLMS-----VHG-VRVRRRNEFFSE---
Cdc27B 238- GIAPPPL-FRNFO-PAVANPNSLITDSSPKSTVNSTLOAPRRKEFVDEGKL

Cdc27A1 280- -ELSAEAQEESEG-RRRSARIAA-----RKKNPMSQSFQKDSHWLHLSP
Cdc27B 286- RKISGRLFSDSGPRR-SSRLSADSGANINSSVATVSGNVNNAASKYLGGSK

SEQ ID NO 12

Cdc27A1 321- SESNYAPSLSSMIGKCRIQSSK-----EAIPD-TV-----TLNDPA
Cdc27B 335- -----LSSLALRS-VTLRKGHSWANENM-DEGVRGEFPDDSRPNTAS

Cdc27A1 356- TTSGQSVSDTGSSVDDEEKSNPSE--SSPDRFSLIS-GISEVLSILKILG
Cdc27B 375- TTGSMASND----QEDETMSIGGIAMSSQT---ITIGVSEILNLLRTLGL

Cdc27A1 403- DGRHLHMYKQEAALLAYOKLSQKQYNTHWVLMQVGKAYFELQDYFNADS
Cdc27B 417- EGCRLSYMYRCQEAALDTYMKLPHKHYNTGWVLSQVGKAYFELIDYLEAEK

Cdc27A1 453- SETLAHQKYPYALEGMDTYSTVLYHLKEEMRLGYLAQELISVDRLSPESW
Cdc27B 467- AERLARLASPYCLEGMDTYSTVLYHLKEDMKLSYLAQELISTDRLAQSW

Cdc27A1 503- CAVGNCYSLRKDHDITALKMFORAIQLNERFTYAHTLCGHEFAALEEFEDA
Cdc27B 517- CAMGNCYSLQKDHETALKNFLRAVQLNPRFAYAHHTLCGHEYTTLDFENG

Cdc27A1 553- ERCYRKALGIDTRHYNAYWGLGMTYLRQEKFEFAQHQFQLALQINPRSSV
Cdc27B 567- MKSYQNALRVDTRHYNAYWGLGMTYLRQEKLEFSEHFERMAFLINPSSSV

Cdc27A1 603- IMCYGIALHESKRNDDEALMMMEKAVLTDKPNPLPKYKKAHILTSIGDYH
Cdc27B 617- IMSYLGTSLHALKRSEEALEIMEQAIVADRKNPLPMYOKANILVCLERLD

Cdc27A1 653- KAQVLEELKECAPQESSVHASL-GKIYNQLKQYDKAVLHFGIALDLSPS
Cdc27B 667- EALEVLEELKEYAPSESSVYA-LMGRIYKRRNMEDKAMLHFGIALDMKPP

SEQ ID NO 7

Cdc27A1 702- PSDAVKIKAYMERLILPDELVTEENL
Cdc27B 716- ATDVAAIKAAMEKLHVPDEIDESP

FIGURE 6

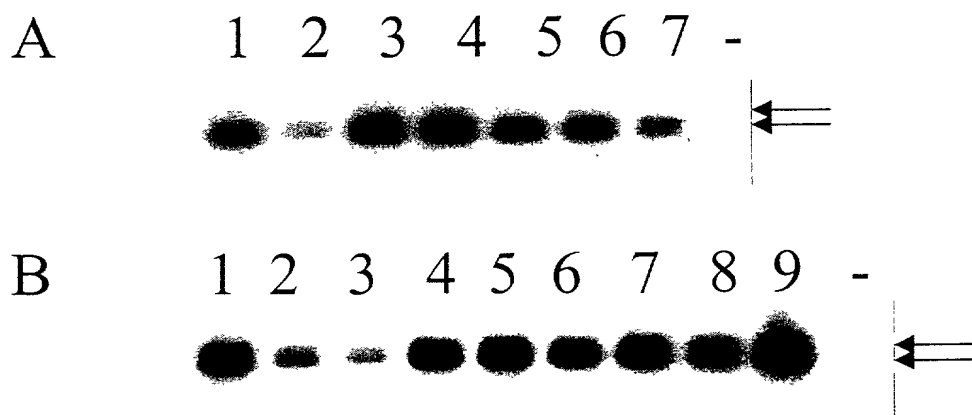


FIGURE 7

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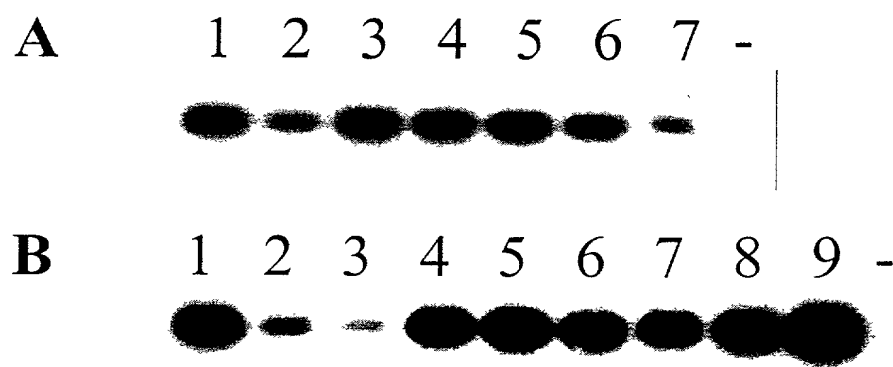


FIGURE 8